

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2003, 06:34:51 ; Search time 46 Seconds
(without alignments)
1688.690 Million cell updates/sec

Title: US-10-091-628-2
Perfect score: 1979
Sequence: 1 MRANSSSSACAPANSSEEL.....FGPMCHRALPVGHTSC 377.

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL 21.*

- 1: sp archaea:*
- 2: sp bacteria:*
- 3: sp fungi:*
- 4: sp human:*
- 5: sp invertebrate:*
- 6: sp mammal:*
- 7: sp mhc:*
- 8: sp organelle:*
- 9: sp phage:*
- 10: sp plant:*
- 11: sp rodent:*
- 12: sp virus:*
- 13: sp vertebrate:*
- 14: sp unclassified:*
- 15: sp virus:*
- 16: sp bacteriophage:*
- 17: sp archaea:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1415	71.5	373	11 Q9CXB2	Q9CXB2 mus musculu
2	871	44.0	348	11 P70172	P70172 mus musculu
3	866	43.8	348	11 Q925U7	Q925U7 mus musculu
4	567.5	28.7	348	6 Q97736	Q97736 oryctolagus
5	546	27.6	317	11 Q35940	Q35940 mus musculu
6	535	27.0	437	4 Q8WU22	Q8WU22 homo sapien
7	535	27.0	462	4 Q96EP9	Q96EP9 homo sapien
8	352	17.8	125	11 Q8V183	Q8V183 mus musculu
9	351.5	17.7	187	11 Q8QZJ2	Q8QZJ2 mus musculu
10	351	16.9	448	4 Q9BSI2	Q9BSI2 mesocricetu
11	333.5	16.4	321	16 Q34524	Q34524 bacillus su
12	325	15.2	305	16 Q99RV2	Q99RV2 staphylococ
13	301.5	15.1	318	16 Q9Y106	Q9Y106 bruceella me
14	299.5	15.1	323	16 Q9KEJ4	Q9KEJ4 bacillus ha
15	284	14.4	338	10 Q81017	Q81017 arabidopsis

17	277	14.0	408	10 Q9AS49	Q9AS49 oryza sativ
18	276	13.9	409	10 Q8S2V7	Q8S2V7 arabidopsis
19	269.5	13.6	311	16 Q9HYX6	Q9HYX6 pseudomonas
20	266.5	13.5	315	16 Q9K0A9	Q9K0A9 neisseria m
21	266.5	13.5	338	17 Q8TPB0	Q8TPB0 methanosaer
22	266	13.4	455	5 Q9VXV4	Q9VXV4 drosophila
23	265.5	13.4	315	16 Q9JVB5	Q9JVB5 neisseria m
24	257.5	13.0	297	16 Q9J375	Q9J375 pseudomonas
25	250	12.6	297	16 Q67889	Q67889 aquifex aeo
26	240	12.1	401	10 Q93YR2	Q93YR2 arabidopsis
27	239	12.1	454	5 Q9VXF5	Q9VXF5 drosophila
28	238.5	12.1	292	16 P73938	P73938 synecocyst
29	230	11.6	325	16 Q9KZG2	Q9KZG2 streptomyce
30	228.5	11.5	313	16 Q8XK10	Q8XK10 salmoneilla
31	223	11.3	207	16 Q8U766	Q8U766 agrobacteri
32	222.5	11.2	318	16 Q9JX64	Q9JX64 neisseria m
33	219.5	11.1	298	16 Q8YLP2	Q8YLP2 anabaena sp
34	211	10.7	111	11 Q91XS4	Q91XS4 mus musculu
35	173	8.7	409	10 Q8VYV4	Q8VYV4 arabidopsis
36	171	8.6	460	10 Q49665	Q49665 arabidopsis
37	170	8.6	273	10 Q94A17	Q94A17 arabidopsis
38	156	7.9	379	10 Q9S268	Q9S268 arabidopsis
39	150	7.6	431	10 Q8RXE8	Q8RXE8 arabidopsis
40	150	7.6	454	10 Q9LSV9	Q9LSV9 arabidopsis
41	142	7.2	344	16 Q86662	Q86662 streptomyce
42	132	6.7	288	17 Q8TWM4	Q8TWM4 methanosaer
43	124	6.3	303	8 Q8SEV7	Q8SEV7 leptura arc
44	121.5	6.1	324	16 Q9X005	Q9X005 thermotoga
45	121	6.1	612	3 Q74395	Q74395 schizosacch

ALIGNMENTS

RESULT 1	Q9CXB2	PRELIMINARY;	PRT;	373 AA.
ID	Q9CXB2			
AC	Q9CXB2			
DT	01-JUN-2001 (TREMREL. 17, Created)			
DT	01-JUN-2001 (TREMREL. 17, Last sequence update)			
DT	01-MAR-2002 (TREMREL. 20, Last annotation update)			
DE	8430417G17RIK protein.			
GN	8430417G17RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=EMBRYONIC LUNG;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batlov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Glaser C., King B., Koehwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Washima J., Mazzaletti U., Mombereis P.,			
RA	Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,			
RA	Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsaki S.,			
RA	Hayashizaki Y.,			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:685-690(2001).			
DR	EMBL; AK018423; BAB31203.1; -			
	MGD; MGI:1923000; 8430417G17RIK.			

DB 183 NHKWPQAKIILKIGSITGVILVILAVIGIILYOSAWIEPKMLIGITPIPIAGSYSGF 242
QY 243 LIALFTHOSWOCRTISLETGAONIOMCTIMLQSFETHVOMLSFPLAYGLFOLLIDGF 302
DB 243 FLARLAGOYWACRVALETGOMOTOLCSTIVOLSSPEDLWVTFPLITVFPQVPA 302
QY 303 LIVAAYQYTKRLKKNHKGKNGSCTEVCHTRKSTSR---ETNAFLEVNEE 350
DB 303 VILGIYVYTRK---CYGNDAEPLE--RTDNEMSRSPFDETNNGFQDDEK 348

RESULT 4

QY 097736 PRELIMINARY; PRT; 348 AA.
AC 097736

DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
Hepatic sodium-dependent bile acid transporter.
Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Stengel S., Becker W., Maier M., Noll R., Kramer W.;
RT "Rabbit cDNA encoding hepatic sodium-dependent bile acid
transporter."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131361; CA10360.1; -
DR InterPro: IPR004710; Bases.
DR InterPro: IPR002657; BileAc/Na_smprtr.
DR Pfam: PF01758; SBF; 1.
DR TIGRfams; TIGR00841; Bases; 1.
SQ SEQUENCE 348 AA; 37932 MW; 992A08F4AAA4489B CRC64;

Query Match 28.7%; Score 567.5; DB 6; Length 348;
Best Local Similarity 38.9%; Pred. No. 8.5e-39;
Matches 112; Conservative 69; Mismatches 100; Indels 7; Gaps 3;

QY 31 ELVFTVSTVMGMLMFLSGSVEIRKLSHRRPWGIAVGLCOFGMLPFTAYLLAISF 90
DB 24 DLATSVILVIMLTIMLSIGCTMEFSKIKAHFLKPGALIALVAQIGIMPLTAFLVGLKF 83
QY 91 SLKPVQALVLMGCCPGGTISNIFTFWDGMDLSMTTGSTVALGMPCLTYLT- 149
DB 84 RKNMTEALAILVCGSPGGMNSNLFSLAVKGMNLSIVMTCTSTFALGMPPLLYISR 143
QY 150 --MSWSLQONLITPYONIGITVCLTIPVAFGVYVYRMPKOSKILKIGAVGVLLV 207
DB 144 GIYEDLKK--VPYIGIMLSLMIIPCTIGIILSKRPQYVYIKVGIITTSISIA 201
QY 208 VAVAGVLAAGSNMSDIT--LLTISFIPFLIGHVTPLLALFTHOSWOCRTISLETGAO 265
DB 202 VAVLSAINVGNISIMYVTPYPLTISALMPFIFGLFISALFRLSARCSRTISMETGQ 261
QY 266 NIGMCTIMQLSTFAHLVQMSFPLAYGLFOLLIDFLLVAAYQYTKR 313
DB 262 NVQLSTILNVTFAPEVIGLFFFPFLYMIQALBGLLIAVRCYCK 309

RESULT 5

QY 035940 PRELIMINARY; PRT; 317 AA.
AC 035940

DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
Na/taurocholate cotransporting polypeptide 2.
GN SLC10A1 OR NTCF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Hagedorn B.;
RT "Identification of two forms of the Na/taurocholate cotransporting
polypeptide in mouse liver."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U95132; AAB81024.1; -
DR MGI; 937379; Slc10a1.
DR InterPro: IPR004710; Bases.
DR InterPro: IPR002657; BileAc/Na_smprtr.
DR Pfam; PF01758; SBF; 1.
DR TIGRfams; TIGR00841; Bases; 1.
SQ SEQUENCE 317 AA; 34886 MW; DA32C829C8ABE6D0 CRC64;

Query Match 27.6%; Score 546; DB 11; Length 317;
Best Local Similarity 37.2%; Pred. No. 4.5e-37;
Matches 118; Conservative 70; Mismatches 117; Indels 12; Gaps 6;

QY 10 ACPANSSEELPVGLEVHGNLEIVTVSTVMGMLMFLSGSVEIRKLSHRRPWGIA 69
DB 7 SAPFNFS--LPFGG-HRATDTALSVILVMLTLIMLSIGCTMEFSKIKAHFWKPKVI 62
QY 70 VGLCOFGMLPFTAYLLAISFSLKPVQALVLMGCCPGGTISNIFTFWDGMDLSISM 129
DB 63 IAIYVQYIMPLSAPFLKGVHLHSIEALILICGCSGNSLFTLAMGDMNLSIVM 122
QY 130 TTGCTVAALGMPCLTYLT--MSWSLQONLITPYONIGITVCLTIPVAFGVYVYRW 186
DB 123 TTCSSFTALGMPPLLYISKGIYDGLKDK--VPYKGMISLVMVLLIPCAIGIFLKSRR 180
QY 187 PKOSKILKIGAVGVLLVAVAGVLAAGSNMSDIT--LLTISFIPFLIGHVTPGL 244
DB 181 PHVYVYKAGNITFSSVAVTVLSTVINGNSIMFWTPHLATTSSLMPTGMLGYIL 240
QY 245 ALFTHOSWOCRTISLETGAONIOMCTIMLQSFETHVOMLSFPLAYGLFOLLIDGFLI 304
DB 241 SALFPLNMSCRTISMETGQVQLCSTIIVTFPEVYIGLFFPFLYMIQALBGLLF 300

QY 305 VAAVQYKRLKKNHKGK 321
DB 301 IIFRCY-LKIKPKQK 316

RESULT 6

QY 08WU22 PRELIMINARY; PRT; 437 AA.
AC 08WU22

DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
Hypothetical 46.5 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019066; AAH19066.1; -
DR InterPro: IPR002657; BileAc/Na_smprtr.
DR Pfam; PF01758; SBF; 1.
DR Hypothetical protein.
SQ SEQUENCE 437 AA; 46503 MW; 055E989629CC13D1 CRC64;

Query Match 27.0%; Score 535; DB 4; Length 437;
Best Local Similarity 35.7%; Pred. No. 5e-36;
Matches 111; Conservative 59; Mismatches 101; Indels 40; Gaps 5;

QY 27 HGNLELVTVVSTVMGMLMFLSGSVEIRKLSHRRPWGIAVGLCOFGMLPFTAYLL 86

```

Db      103 HGNLNFVGAALCTTMMG-----LGCTVDVNHFGAHRPRPGALLAALCOFGLPLLAFL 157
Qy      87 AIFSFLKPVQALAVLIMGCCPGGTINIFFWVDGMDLSISWTCSTVAALGMPFLCY 146
      158 ALAFKIDEVAAVAVLLCGCGPGNLSNLSLVDGDMNSIITISTTLALVLMPLCLM 217
Db      147 LYTWSN---SLOQNLTPYQNIITLVCLTTPVAFGVYVYVYRMPKSKIIKI----- 196
      218 IYSWAINPIVQ--LLPLGTVTLTLCSTLPIGLGVFRKYSRVADYIVKXSLMSLLV 275
Qy      197 -----GAVVGVLVAVAVAGVVLAKGSWNSDITLTTISFIPLIGHVTFGLALF 247
      276 TLVVLFIPTMTGMPBLASIPAAVYIA-----IFMPLAGVAGYGLATL 321
Db      248 THOSMORCRTISLETGAQNIOMCTIMQLSFTAHLVOMLSFPLAYGLFQILDGFLI 307
      322 FLHPKCKRTVCLETSGNQVQLCTAILKLAFPPQFISGMVFPFLYALFQSAEAGIFVLI 381
Qy      308 YQTYKRLKXK 318
      382 YKMGSEMLHK 392

```

RESULT 7

```

Q96EP9 ID Q96EP9 PRELIMINARY; PRT; 462 AA.
AC 096EP9;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Unknown (Protein for IMAGE:3502817) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Strausberg R.;
RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC012048; AAH12048.1; -
DR InterPro; IPR002657; BileAc/Na_smptr.
DR Pfam; PF01758; SBF; 1.
FT NON_TER
SQ SEQUENCE 462 AA; 49035 MW; B916D68AE40622C CRC64;

```

Query Match 27.0%; Score 535; DB 4; Length 462;

Best Local Similarity 35.7%; Pred. No. 5.3e-36; Mismatches 101; Indels 40; Gaps 5;

```

Matches 111; Conservative 59; Mismatches 101; Indels 40; Gaps 5;
Qy      27 HGNLIEVFTVSTVMGMLMFSIGCSVEIRKLSHRRPWGIVAGLLCOFGLMPTAYLL 86
      128 HGNLNFVGAALCTTMMG-----LGCTVDVNHFGAHRPRPGALLAALCOFGLPLLAFL 182
Db      87 AIFSFLKPVQALAVLIMGCCPGGTINIFFWVDGMDLSISWTCSTVAALGMPFLCY 146
      183 ALAFKIDEVAAVAVLLCGCGPGNLSNLSLVDGDMNSIITISTTLALVLMPLCLM 242
Qy      147 LYTWSN---SLOQNLTPYQNIITLVCLTTPVAFGVYVYVYRMPKSKIIKI----- 196
      243 IYSWAINPIVQ--LLPLGTVTLTLCSTLPIGLGVFRKYSRVADYIVKXSLMSLLV 300
Db      197 -----GAVVGVLVAVAVAGVVLAKGSWNSDITLTTISFIPLIGHVTFGLALF 247
      301 TLVVLFIPTMTGMPBLASIPAAVYIA-----IFMPLAGVAGYGLATL 346
Qy      248 THOSMORCRTISLETGAQNIOMCTIMQLSFTAHLVOMLSFPLAYGLFQILDGFLI 307
      347 FLHPKCKRTVCLETSGNQVQLCTAILKLAFPPQFISGMVFPFLYALFQSAEAGIFVLI 406
Db      308 YQTYKRLKXK 318
      382 YKMGSEMLHK 392

```

Db 407 YKMGSEMLHK 417

RESULT 8
ID 08V183 PRELIMINARY; PRT; 125 AA.

```

AC 08V183;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Ilean sodium-dependent bile acid transporter (Fragment).
CN ISBT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Saeki T., Kirifuji K., Kanamoto R., Iwami K.;
RT "Identification of transcription start sites in mouse ileal sodium-
RT dependent bile acid transporter gene."
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB078635; BAB84081.1; -
DR InterPro; IPR002657; BileAc/Na_smptr.
DR Pfam; PF01758; SBF; 1.
FT NON_TER
SQ SEQUENCE 125 AA; 13275 MW; C7F8EFC459D4C8F7 CRC64;

```

Query Match 17.8%; Score 352; DB 11; Length 125;

Best Local Similarity 52.0%; Pred. No. 1.5e-21; Mismatches 64; Conservative 25; Mismatches 30; Indels 4; Gaps 2;

```

Qy      7 SSSACPNASS--EEELPYGLEVHGN--LELVFTVSTVMGMLMFSIGCSVEIRKLSHI 62
      3 NSSVCPNATVCEGSDCVPEESFNALINTVASTVLTILAMVPMSCNEVHFKLGH 62
Qy      63 RRPWGIVAGLLCOFGLMPTAYLLAIFSFLKPVQALAVLIMGCCPGGTINIFFWVDG 122
      63 KRPWGI FVGLCOFGLMPTAYLLAIFSFLKPVQALAVLIMGCCPGGTINILAYWIDG 122
Db      123 MDL 125
      123 MDL 125

```

RESULT 9

Q8QZR2 PRELIMINARY; PRT; 473 AA.

```

AC 08QZR2;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Similar to protein p3 (Hypoetical 50.3 kDa protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC027440; AAH27440.1; -
DR EMBL; BC027440; AAH27440.1; -
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 50254 MW; 9A2ADDA005DD1805 CRC64;

```

Query Match 17.8%; Score 351.5; DB 11; Length 473;

Best Local Similarity 32.4%; Pred. No. 6.4e-21; Mismatches 91; Conservative 57; Mismatches 108; Indels 25; Gaps 5;

QY 11 CPANSEELPYGLEVH-GNLE--LVFTVSTVMGMLMFSIGCSVEIRKLSHRRPM 66
 DB 163 CIRVSPARELPSALNTNIGHFSENPFLVLLPLIFPNKSF--GCNVELEVKELOISQ 220
 QY 67 GIAGVLLCGFGLMPFAYLLAISFSIKPVOAIVLMGCCPGGTTISNFTFWVDGMDLS 126
 DB 221 PMLLGLGGLVMPFYAFIMAKVFMPLKALALGLIITCSSPGGGGSYFLSLGGDVTLA 280
 QY 127 ISMTCSYTAALGMPCLITYTWSLQOONTIPQONIGITLVCLITIVAGVYVNRK 186
 DB 281 ISMTFISTVAATGFLPLSSAIVSYLLSIHETLHPISKILGLFLFAIPAGVYIKSL 340
 QY 187 PKOSKIILKIGAVGVLL-----VVAAGVVLAKGSWNSDITLITISFIFPL 236
 DB 341 PFESELLQVIRKPFSTILLGLFLAYHMGVFLVGR-----PIVLGVFTVPLV 391
 237 GHVTFLLALFTHQSWORCRITSLGTGQONIQMTLMQLS 277
 392 GLVGVSLALCLKLPVAGRRVTSIEGVQNSLLALAMQLS 432

RESULT 10

Q9QZJ2 PRELIMINARY; PRT; 187 AA.

AC Q9QZJ2; PRELIMINARY; PRT; 187 AA.
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAY-2002 (TREMblrel. 20, Last annotation update)
 DE Na-Tauchocholate cotransporting polypeptide (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mesocricetus.
 NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Balasubramanian N., Arrese M., Suchy F.J., Ananthanarayanan M.;
 RT "Na-Tauchocholate cotransporting polypeptide (Ntcp) from Hamster
 RT liver".
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF181258; AAD53961.1;
 DR InterPro; IPR002657; BileAc/Na_smprtr.
 DR Pfam; PF01758; SBF; 1.
 FT NON_TER 1, 187
 NON_TER 187
 SEQUENCE 187 AA; 20182 MW; 2855C5F44AB482C6 CRC64;

Query Match 17.7%; Score 351; DB 11; Length 187;
 Best Local Similarity 42.6%; Pred. No. 2.8e-21;
 Matches 80; Conservative 34; Mismatches 64; Indels 10; Gaps 5;

QY 75 QGIMPFAYLLAISFSIKPVOAIVLMGCCPGGTTISNFTFWVDGMDLSISMTTCT 134
 DB 1 QGIMPLAFVGVKGFHLKPIBALAILICGSPGGLNSLFLAMGDMNLSIVMTTCT 60
 QY 135 VVALGMPCLITYLT---WSNLSQONTIPYONIGITLVCLITPAFVGVYVNRPKQSK 191
 DB 61 FVALGMPCLITYLT---WSNLSQONTIPYONIGITLVCLITPAFVGVYVNRPKQSK 118
 QY 192 ILIKIGAVGVLLVAVAGVVLAKGSWNSDIT--LTITISFIFPLIGHVTFLL-ALPT 248
 DB 119 YIIKGMITTFILSAVAVVLSIINNGNSIKFAMTPPLATSSLMPSGFLGALSALF- 177
 QY 249 HQSQQR 256
 DB 178 -OLNPRCR 184

RESULT 11
 Q9BSL2 PRELIMINARY; PRT; 448 AA.
 AC Q9BSL2;

DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Similar to protein p3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC004966; AA004966.1;
 DR InterPro; IPR004710; Baas.
 DR InterPro; IPR002657; BileAc/Na_smprtr.
 DR Pfam; PF01758; SBF; 1.
 DR TIGRFAMs; TIGR00841; baas; 1.
 SO SEQUENCE 448 AA; 47548 MW; 47A1263CF8EFPF91 CRC64;

Query Match 16.9%; Score 333.5; DB 4; Length 448;
 Best Local Similarity 31.5%; Pred. No. 1.8e-19;
 Matches 87; Conservative 53; Mismatches 115; Indels 21; Gaps 3;

QY 12 PANSEELPYGLEVHGNLELVFTVSTVMGMLMFSIGCSVEIRKLSHRRPMGIAGV 71
 DB 143 PAEDPATLSADLAFSENPFLVLLPLIFPNKSF--GCNVELEVKELOISQ 200
 QY 72 LLQGLMPFAYLLAISFSIKPVOAIVLMGCCPGGTTISNFTFWVDGMDLSISMT 131
 DB 201 LLQGLVMPFLVAFIMAKVFMPLKALALGLIITCSSPGGGGSYFLSLGGDVTLAISMT 260
 QY 132 CSTVALGMPCLITYTWSLQOONTIPYONIGITLVCLITPAFVGVYVNRPKQSK 191
 DB 261 LSTVAATGFLPLSSAIVSYLLSIHETLHPISKILGLFLFAIPAGVYIKSKPKFSQ 320
 QY 192 ILIKIGAVGVLL-----VVAAGVVLAKGSWNSDITLITISFIFPLIGHV 241
 DB 321 LLQGVKPFSTILLGLFLAYHMGVFLVGR-----PIVLGVFTVPLVGLV 371
 QY 242 FLALFTHQSWORCRITSLGTGQONIQMTLMQLS 277
 DB 372 YCLATCLKLPVAGRRVTSIEGVQNSLLALAMQLS 407

RESULT 12

Q34524 PRELIMINARY; PRT; 321 AA.

AC Q34524; PRELIMINARY; PRT; 321 AA.
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Putative translocator.
 GN YOCs.
 OS Bacillus subtilis.
 CC Bacteria; Firmicutes; Bacillales; Clostridium group; Bacillales;
 CC Bacillaceae; Bacillus.
 NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lapidus A., Galleron N., Sorokin A., Ehrlich D.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Berteiro M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Funa S., Gallizzi A., Galleron N.,
 RA Ghim S.Y., Glaeser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henat A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Jorja B., Karamata D., Kasahara Y., Klaer-Bianchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapides A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Malet C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogilwara A., Oudega B., Park S.H.,
 RA Paro V., Pohl T.M., Portetelle D., Portollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scottone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
 RA Sorokin A., Taccini E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terstra P., Togomi A.,
 RA Tostato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambuit R., Wedler E., Wedler H., Weitenegger T.,
 RA Winters P., Wipf A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumsstein E., Yoshikawa H., Danchin A.,
 "The complete genome sequence of the gram-positive bacterium *Bacillus subtilis*."
 sub118.";
 RL Nature 390:249-256(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kuner F., Ogasawara N., Yoshikawa H., Danchin A.,
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF027868; AAB8443.1; -.
 DR EMBL: Z29114; CAB13827.1; -.
 DR InterPro: IPR004710; Baa5.
 DR InterPro: IPR002657; BileAc/Na_smptr.
 DR Pfam: PF01758; SBF; 1.
 DR TIGRfams: TIGR00841; Baa5; 1.
 KW Complete proteome.
 SQ SEQUENCE 321 AA; 34251 MW; 0D9CCFB3E84A96 CRC64;
 Query Match 16.4%; Score 325; DB 16; Length 321;
 Best Local Similarity 27.6%; Pred. No. 6.5e-19;
 Matches 84; Conservative 76; Mismatches 114; Indels 30; Gaps 12;
 QY 33 VPTVVS---TWMMGLMFSIGCSVEIRKLSHRRWGVIAVGLCPGMPFTAYLAIS 89
 DB 32 LFTWISSYITFTFGITMFGWGLTLDDEKELVRKQVQVIGVIAQYTTMPLVAFGLA 91
 QY 90 FSLKPVQALVAVLMGCCPGGTTISNFTFWVDGMDISMTTCTVAALGMPLCIYLYT 149
 DB 92 LHLPAIAGVILVCGCGPGTASNNWTFIAKGNFTALSAVATTSTILAPVTPPLIML 151
 QY 150 WSWSLQONTLTPYQNGITLV-CLTTPVAGVYVYVYVYVYVYVYVYVYVYVYVYV 205
 DB 152 KEW-----LPVSPGSFISITLQAVLPFIAGLIVKMFPRQVAKAVHALPLVSV 202
 QY 206 LVAVAVGVVLAKSNM---SDITLITISFIFPLIGVITGLALFTHQSMQRCRTISL 262
 DB 203 -IVAVISAVASGNREVLQSLGILFISVILHNGIGLGLCKLKMIDPSOKAIAIV 261
 QY 263 GAQNIQMTIMLTQSTFAEHLVQMLSFPLA-YGLPOLIDGFLIVAAVQYTKRLKHKH-G 320
 DB 262 GNQN-----SGLGAALATAHFSLVSAVPSAIFSVHNLGSKML-ATY--WSKVKVKKQ 313
 QY 321 KKNK 324
 DB 314 SKKS 317

DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
 DE Hypothetical protein SAV2321.
 GN SAV2321 OR SA2112.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Clostridium group; Bacillales;
 OC Staphylococcus.
 NX NCB1_Taxid=158878; 158879;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S. aureus (strain Mu50), and S. aureus (strain N315);
 RX MEDLINE=2111952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanemori M., Matsumaru H., Matuyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yaburaki J.,
 RA Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hatori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*."
 RT Lancet 357:1225-1240(2001).
 RL EMBL: AP003365; BAB58483.1; -.
 DR EMBL: AP003365; BAB58483.1; -.
 DR InterPro: IPR002657; BileAc/Na_smptr.
 DR Pfam: PF01758; SBF; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 305 AA; 32865 MW; 1E423015196B657 CRC64;
 Query Match 15.2%; Score 301.5; DB 16; Length 305;
 Best Local Similarity 27.9%; Pred. No. 5.3e-17;
 Matches 68; Conservative 60; Mismatches 101; Indels 15; Gaps 4;
 QY 41 NMGLMFSIGCSVEIRKLSHRRWGVIAVGLCPGMPFTAYLAISFSLKPVQALV 100
 DB 41 LGLVLMGLMGLTITNDPRKVPKAPRAVILVGLCPGMPFTAYLAISFSLKPVQALV 100
 QY 101 LMGCCPGGTTISNFTFWVDGMDISMTTCTVAALGMPLCIYLYTWSLQONTL 160
 DB 101 ILVGGCPGTTISNFTFWVDGMDISMTTCTVAALGMPLCIYLYTWSLQONTL 160
 QY 161 PYQNGITLVCLTTPVAGV---YVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 214
 DB 161 LMSVQVAVL---LFAAGVYQIIRKIAEASTALPISVAISLAIYVGGSKQI 216
 QY 215 IAKGSWSDITLITISFIFPLIGVITGLALFTHQSMQRCRTISLGAQNIQMTIML 274
 DB 217 LTTG-----LIFLVIIHNVLYGTITGLVRLKLTLDQDQKAVSIEVGMQNSGLAVSL 271
 QY 275 QLSF 278
 DB 272 ALHF 275
 RESULT 14
 ID 08YIU6 PRELIMINARY; PRT; 318 AA.
 AC 08YIU6;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Sodium/bile acid cotransporter homolog, SBF family.
 GN BME10346.
 OS *Brucella melitensis*.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 NX NCB1_Taxid=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA Delvecchio V.G., Kapral V., Redkar R.J., Patra G., Mujeer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,

THIS PAGE BLANK (USPTO)